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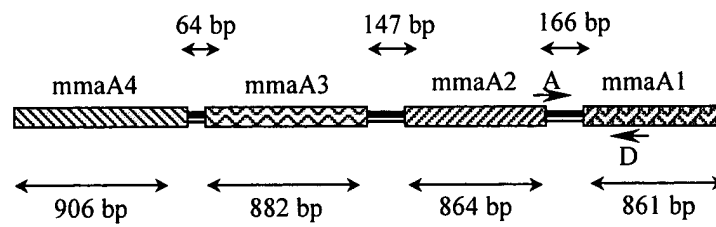
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**Figure 1:** Schematic diagram of methoxy mycolic acid synthase mmaA 4-mmaA 1 gene cluster of mycobacteria and location of forward A, and reverse D primers.

CTACTTCGCCAGCGTGAACTGGTTGACGTGCGATGTAGCCGACCCGGAAACAGCTTGGCGCAGCCGGTCAGGTATTTTC  
 ATGTACCGCTCGTAGACCTCTTCGGACTGGATCGCGATGGCCCTCGCTTTTGTGTCTCTGCAGCGCCTCGGCCACAG  
 GTCGAGGGTCTCTGGCGTAATGCGGGCTGCAGCGACTGGCGGCGAGTCAGCGTGAAACCCGTCTTCGCCGACTGTTCC  
 TCAACCATTTCAATCGTCGGAGGTTGGCCCCCCCCGGGAAGATTTCGGTCGCGATGAACCTTGAGAAAGCGGGCCAGCC  
 ACAACGTGAGCGGAAGCCGTGGTCGACCATCTGCTGCCTGGTCAGGCCGGTGATCGTGTGACAGCAACACGCG  
 CATCGGCGGACAGGATTTTGTGGCCCCGGCGAAGATCGGCGTGACGATCGTGGCCGAAGTGCTCGAAACGCGC  
 CGATCGACACGATGCGGTGCGACGGGCTCGTTGAACCTGCTCCCATCCCGCCAGCAACACTCGCCTGTCTCGCGGGGT  
 GTCCATCTGTCGAACGACTTCTGCACATGGCGGGCTGGTTCTTCGACAATGTCAGGCCGACGAGTTGACGTCA  
 TACTGCGGATCGCGCGCCGATGTTGGCGCCCCAGCCGCAACCGATATCGAGCAGCGTCAATGCCGGCTGCAGA  
 CCTAGCTTGCCAGCGCAGGTCGATCTTGGCGATCTTGGCCCTCTTCCAGCGTCATGCTCGCGTTCGAAATGCGC  
 GCAGCTGTAGGTCTGGGTCCGATCCAGGAACAGCCGGAAGAAAGTCGTCGGACAGGTCGTAGTGTGCCTGCACGTC  
 CTCGAAAGTGGCGGTTAGGTCTGTTGACCAATgagggtgaaagcttcccgaccctaggtggcttcgttgcaaggaaacgacgatgtccccctcccc  
 gcatctcgaaggcatctatccgatacagggccgcgcactaaaccgacgacgaattgcccaggtcagggaacgagatagcggacgagCTACTTGGTCAATGGTGAA  
 CTGGGCGACGTTGATTAGGCCCTCTGCGGAAGCGCTCCGCGCATCCCGTCAGATAGTGCAATGAAGTTGTTGTAGACC  
 TCTTCGGACTGTACGGCGATGGCGCGTTTCGCGGCGAGCCTGTAGGTTGGCGGCCCATGCAATCGAGATGTCGGGCTCCGAT  
GTGCTGCTGCAGCAGCTGGACATGCTCGATGTTGAAGCCCGGGCCTGCGCATTTGTCGACAAATGTCGGGCTCCGAT  
 GGCAGCTCGCCCGCGGAAGATCGACTCCCGCAGGAATTTGAGGAATCGAAGTCCGTCATCGTCAGCGCAATG  
 CCCTGTTCTGTCAGCCACCTGCGGTGCTAGGTGAACAGGCTGTGCAGTAGCATCCGCCCGTCATCGGGCAGGATGT  
 CGTAGGAGCGTTCGAAGAACGTCAGATACCGCTCCTTTTGAACGCGTCGAATGCCTCAAAGCTGACGATCCCGTC  
 GACGTTCTTCAAACTCTTCCCAGCCCTGCAGCCGGCTCGCGCGCCGTTGCGTTCCGATTCGATTCGCGCCAGGCGG  
 TCTTTGCTGCGTTCATAGTATTCCGGCTGAGCGTGAGGCCGATGACATTGACGTCGTACTTCTCCACGGCCCCGAAC  
 GAGCGCCCCCCCCACCCGCAACCCACGTCGAGTAGCGTCAATCCCCGGTTTCGAGGTTTCAGCTTGTCCAACGCCAGA  
 TCCACCTTGCCAGTTGCGCCTCTTCCAGCGTCATATCGTCACGCTCGAAATAGCGCAGGTGTAGACCCAGGTGG  
 GATCGAGGAACAACGCGAAGAAAGTCATCCGAAATGTCGTAAGCCGACTGTGACTCTTCGTAATATGTTCTCAGCTT  
 GGCCAT

**Fig. 2:** Sequence of *mmaA2* and *mmaA1* gene with an intergenic region of 166 base pair (shown in lower case. Location of forward A, sequence ID 1 and reverse primer D, sequence ID 2. Both primer sequence is underlined and italicized.

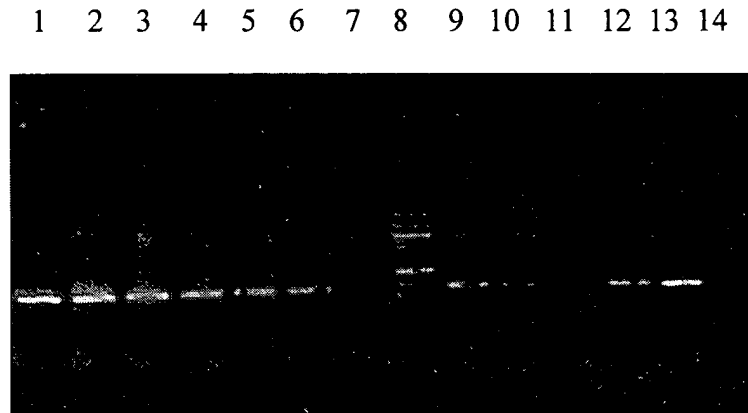
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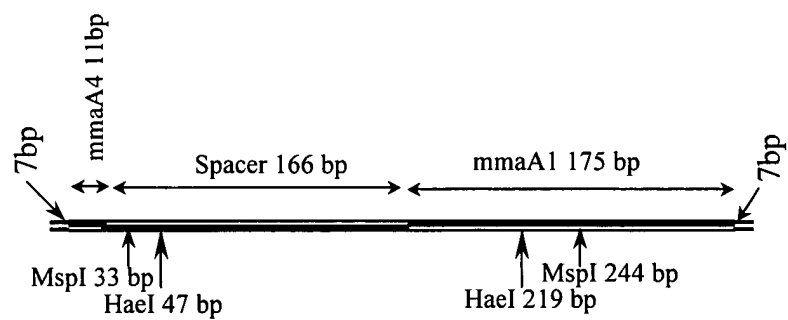
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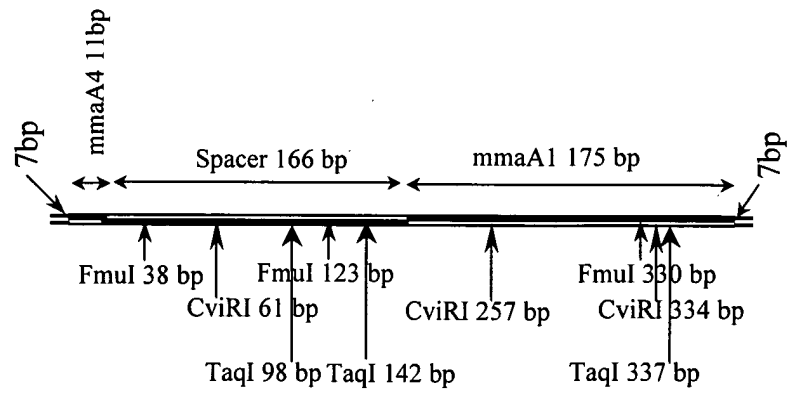
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**Fig. 3** PCR amplification of different mycobacterial genomic DNAs with primers A and D (lanes 1- 15): 1. *M.avium* 2. *M.bovis* 3. *M.chelonae* 4. *M.fortuitum* 5. *M.intracellulare* 6. *M.kansassi* 7. *M.phlei* 8. 100 bp DNA ladder 9. *M.marinum* 10. *M.scrofulaceum* 11. *M.smegmatis* 12. *M.szulgai*, 13. *M.tuberculosis* and 14. negative control. AD indicates 363 bp-amplified product.



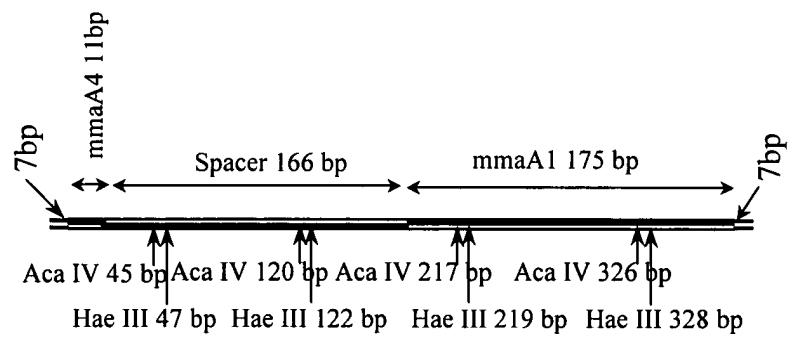
**Fig. 4:** line diagram showing restriction endonuclease map of HaeI and MspI within AD.



**Fig. 5:** line diagram showing restriction endonuclease map of Fmul, CviRI and TaqI within AD.

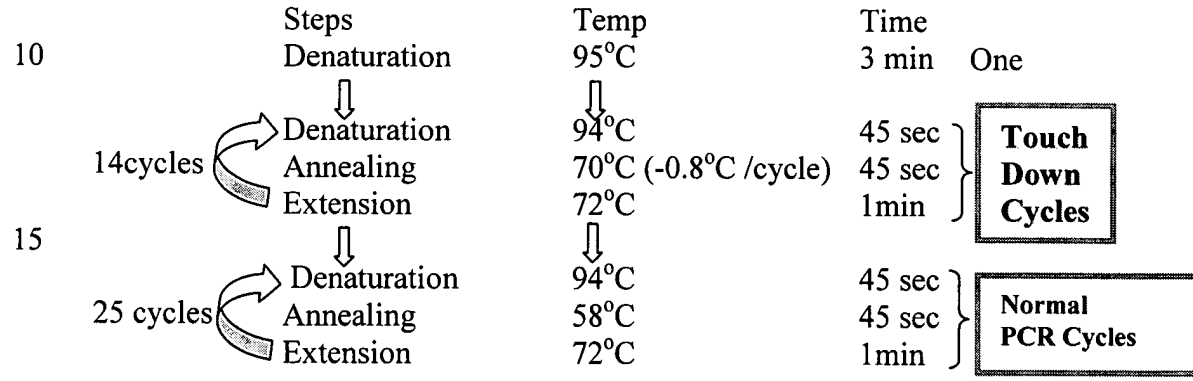
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**Fig. 6:** Restriction map of AD showing distribution of the sites of restriction endonucleases AcaIV and HaeIII.

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**Fig. 7:** Line diagram showing different steps of PCR reaction